

Figure 1

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| | 32a ⚡ | 32b ⚡ | 32c ⚡ |
|-------|----------------|-------------------------------|---------------------------------|
| | Atom-Pair Type | Distance Value (Angstroms) | Well-Depth Value (-kcal/mol) |
| 34a ~ | CF-CO | 4.2 | 0.1917 |
| 34b ~ | CF-CN | 4.2 | 0.3797 |
| 34c ~ | CF-NC | 3.55 | 0.4225 |
| 34d ~ | CF-NP | 4.2 | 0.3025 |
| 34e ~ | CP-OA | 3 | 0.4325 |
| 34f ~ | NC-CO | 3.8 | 1.4381 |
| 34g ~ | OC-OD | 2.6 | 1.4604 |
| 34h ~ | OA-ND | 2.9 | 0.7225 |
| 34i ~ | SA-NR | 4.4 | 0.6577 |

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Figure 2

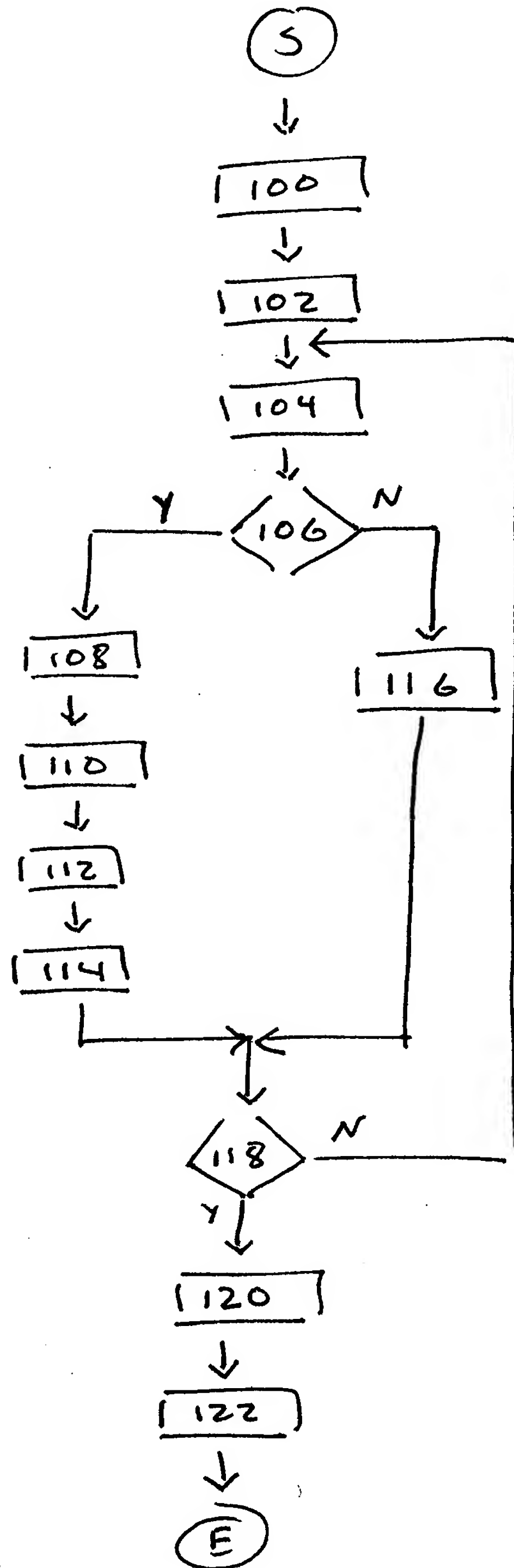


Figure 3

100. USER SPECIFIES PROTEIN-LIGAND COMPLEX
102. PMF-SCORING MODULE ACCESSES PMF-SCORING DATA ASSOCIATED WITH SPECIFIED PROTEIN-LIGAND COMPLEX
104. PMF-SCORING MODULE IDENTIFIES PROTEIN-LIGAND ATOM PAIR IN SPECIFIED PROTEIN-LIGAND COMPLEX
106. SHOULD REPULSION TERM BE USED TO CALCULATE PMF OF IDENTIFIED PROTEIN-LIGAND ATOM PAIR?
108. PMF-SCORING MODULE ACCESSES TABLE OF EMPIRICALLY DERIVED MINIMUM BINDING-ENERGY DISTANCE AND WELL-DEPTH VALUES
110. PMF-SCORING MODULE USES ACCESSED TABLE TO DETERMINE A MINIMUM BINDING-ENERGY DISTANCE VALUE AND A WELL-DEPTH VALUE THAT CORRESPOND TO IDENTIFIED PROTEIN-LIGAND ATOM PAIR
112. PMF-SCORING MODULE USES DETERMINED MINIMUM BINDING-ENERGY DISTANCE AND WELL-DEPTH VALUES TO CALCULATE REPULSION TERM
114. PMF SCORING MODULE USES CALCULATED REPULSION TERM TO CALCULATE PMF OF IDENTIFIED PROTEIN-LIGAND ATOM PAIR
116. PMF SCORING MODULE CALCULATES PMF OF IDENTIFIED PROTEIN-LIGAND ATOM PAIR WITHOUT REPULSION TERM
118. PMF CALCULATED FOR EVERY PROTEIN-LIGAND ATOM PAIR IN SPECIFIED PROTEIN-LIGAND COMPLEX?
120. PMF-SCORING MODULE USES CALCULATED PMFs TO CALCULATE PMF SCORE OF SPECIFIED PROTEIN-LIGAND COMPLEX
122. PMF-SCORING MODULE COMMUNICATES CALCULATED PMF SCORE TO USER

Figure 3 (continued)